

Figure 1

□□□□□□□□□□□□□□□□□□

ATG TCA AAT ATT ACA GAT CCA CAG ATG TGG GAT TTT 86
Met Ser Asn Ile Thr Asp Pro Gln Met Trp Asp Phe
1 5 10

5 GAT GAT CTA AAT TTC ACT GGC ATG CCA CCT GCA GAT GAA 125
Asp Asp Leu Asn Ph Thr Gly Met Pro Pro Ala Asp Glu
15 20 25

10 GAT TAC AGC CCC TGT ATG CTA GAA ACT GAG ACA CTC AAC 164
Asp Tyr Ser Pro Cys Met Leu Glu Thr Glu Thr Leu Asn
30 35

15 AAG TAT GTT GTG ATC ATC GCC TAT GCC CTA GTG TTC CTG 203
Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu Val Phe Leu
40 45 50

20 CTG AGC CTG CTG GGA AAC TCC CTG GTG ATG CTG GTC ATC 242
Leu Ser Leu Leu Gly Asn Ser Leu Val Met Leu Val Ile
55 60

25 TTA TAC AGC AGG GTC GGC CGC TCC GTC ACT GAT GTC TAC 281
Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr
65 70 75

30 CTG CTG AAC CTG GCC TTG GCC GAC CTA CTC TTT GCC CTG 320
Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu
80 85 90

35 ACC TTG CCC ATC TGG GCC GCC TCC AAG GTG AAT GGC TGG 359
Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp
95 100

40 ATT TTT GGC ACA TTC CTG TGC AAG GTG GTC TCA CTC CTG 398
Ile Phe Gly Thr Phe Leu Cys Lys Val Val Ser Leu Leu
105 110 115

45 AAG GAA GTC AAC TTC TAC AGT GGC ATC CTG CTG TTG GCC 437
Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu Leu Leu Ala
120 125

50 TGC ATC AGT GTG GAC CGT TAC CTG GCC ATT GTC CAT GCC 476
Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His Ala
130 135 140

55 ACA CGC ACA CTG ACC CAG AAG CGT CAC TTG GTC AAG TTT 515
Thr Arg Thr Leu Thr Gln Lys Arg His Leu Val Lys Phe
145 150 155

50 GTT TGT CTT GGC TGC TGG GGA CTG TCT ATG AAT CTG TCC 554
Val Cys Leu Gly Cys Trp Gly Leu Ser Met Asn Leu Ser
160 165

55 CTG CCC TTC TTC CTT TTC CGC CAG GCT TAC CAT CCA AAC 593
Leu Pro Phe Phe Leu Phe Arg Gln Ala Tyr His Pro Asn
170 175 180

AAT TCC AGT CCA GTT TGC TAT GAG GTC CTG GGA AAT GAC 632

Fig. 2a

□□□□□□□□□□□□□□□□□□

		Asn Ser Ser Pro Val Cys Tyr Glu Val Leu Gly Asn Asp
		185 190
5		ACA GCA AAA TGG CGG ATG GTG TTG CGG ATC CTG CCT CAC 671 Thr Ala Lys Trp Arg Met Val Leu Arg Ile Leu Pro His 195 200 205
10		ACC TTT GGC TTC ATC GTG CCG CTG TTT GTC ATG CTG TTC 710 Thr Phe Gly Phe Ile Val Pro Leu Phe Val Met Leu Phe 210 215 220
		TGC TAT GGA TTC ACC CTG CGT ACA CTG TTT AAG GCC CAC 749 Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His 225 230
15		ATG GGG CAG AAG CAC CGA GCC ATG AGG GTC ATC TTT GCT 788 Met Gly Gln Lys His Arg Ala Met Arg Val Ile Phe Ala 235 240 245
20		GTC GTC CTC ATC TTC CTG CTT TGC TGG CTG CCC TAC AAC 827 Val Val Leu Ile Phe Leu Leu Cys Trp Leu Pro Tyr Asn 250 255
25		CTG GTC CTG CTG GCA GAC ACC CTC ATG AGG ACC CAG GTG 866 Leu Val Leu Leu Ala Asp Thr Leu Met Arg Thr Gln Val 260 265 270
30		ATC CAG GAG ACC TGT GAG CGC CGC AAC AAC ATC GGC CGG 905 Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg 275 280 285
		GCC CTG GAT GCC ACT GAG ATT CTG GGA TTT CTC CAT AGC 944 Ala Leu Asp Ala Thr Glu Ile Leu Gly Phe Leu His Ser 290 295
35		TGC CTC AAC CCC ATC ATC TAC GCC TTC ATC GGC CAA AAT 983 Cys Leu Asn Pro Ile Ile Tyr Ala Phe Ile Gly Gln Asn 300 305 310
40		TTC CGC CAT GGA TTC CTC AAG ATC CTG GCT ATG CAT GGC 1022 Phe Arg His Gly Phe Leu Lys Ile Leu Ala Met His Gly 315 320
45		CTG GTC AGC AAG GAG TTC TTG GCA CGT CAT CGT GTT ACC 1061 Leu Val Ser Lys Glu Phe Leu Ala Arg His Arg Val Thr 325 330 335
50		TCC TAC ACT TCT TCG TCT GTC AAT GTC TCT TCC AAC CTC 1100 Ser Tyr Thr Ser Ser Ser Val Asn Val Ser Ser Asn Leu 340 345 350
		TGAAACCAT CGATGAAGGA ATATCTCTTC TCAGAAGGAA AGAATAACCA 1150
55		ACACCCCTGAG GTGTGTGTG GAAGGTGATC TGGCTCTGGA CAGGCACTAT 1200
		CTGGGGTTTG GGGGGACGCT ATAGGAIGTG GGGAAAGTTAG GAACTGGTGT 1250

Fig. 2b

□ 9 1 0 4 0 6 9 □ 0 6 2 1 9 8

CTTCAGGGGC CACACCAACC TTCTGAGGAG CTGTTGAGGT ACCTCCAAGG 1300
5 ACCGGCCTTT GCACCTCCAT GGAAACGAAG CACCATCATT CCCGTTGAAC 1350
10 GTCACATCTT TAACCCACTA ACTGGCTAAT TAGCATGGCC ACATCTGAGC 1400
15 CCCGAATCTG ACATTAGATG AGAGAACAGG GCTGAAGCTG TGTCTCATG 1450
20 AGGGCTGGAT GCTCTCGTTG ACCCTCACAG GAGCATCTCC TCAACTCTGA 1500
25 GTGTTAAGCG TTGAGCCACC AAGCTGGTGG CTCTGTGTGC TCTGATCCGA 1550
30 GCTCAGGGGG GIGGTTTCC CATCTCAGGT GTGTTGCAGT GTCTGCTGGA 1600
35 GACATTGAGG CAGGCACCTGC CAAACATCA ACCTGCCAGC TGGCCTGTG 1650
40 AGGAGCTGGA AACACATGTT CCCCTGGGG GTGGTGGATG AACAAAGAGA 1700
30 AAGAGGGTTT GGAAGCCAGA TCTATGCCAC AAGAACCCCC TTTACCCCCA 1750
35 TGACCAACAT CGCAGACACA TGTGCTGGCC ACCTGCTGAG CCCCAAGTGG 1800
40 AACGAGACAA GCAGCCCTTA GCCCTCCCCC TCTGCAGCTT CCAGGCTGGC 1850
GTCAGCATC AGCATCCCTA GAAAGCCATG TGCAGCCACC AGTCCATTGG 1900
40 GCAGGCAGAT GTTCTTAATA AAGCTTCTGT TCC 1933

Fig. 2c

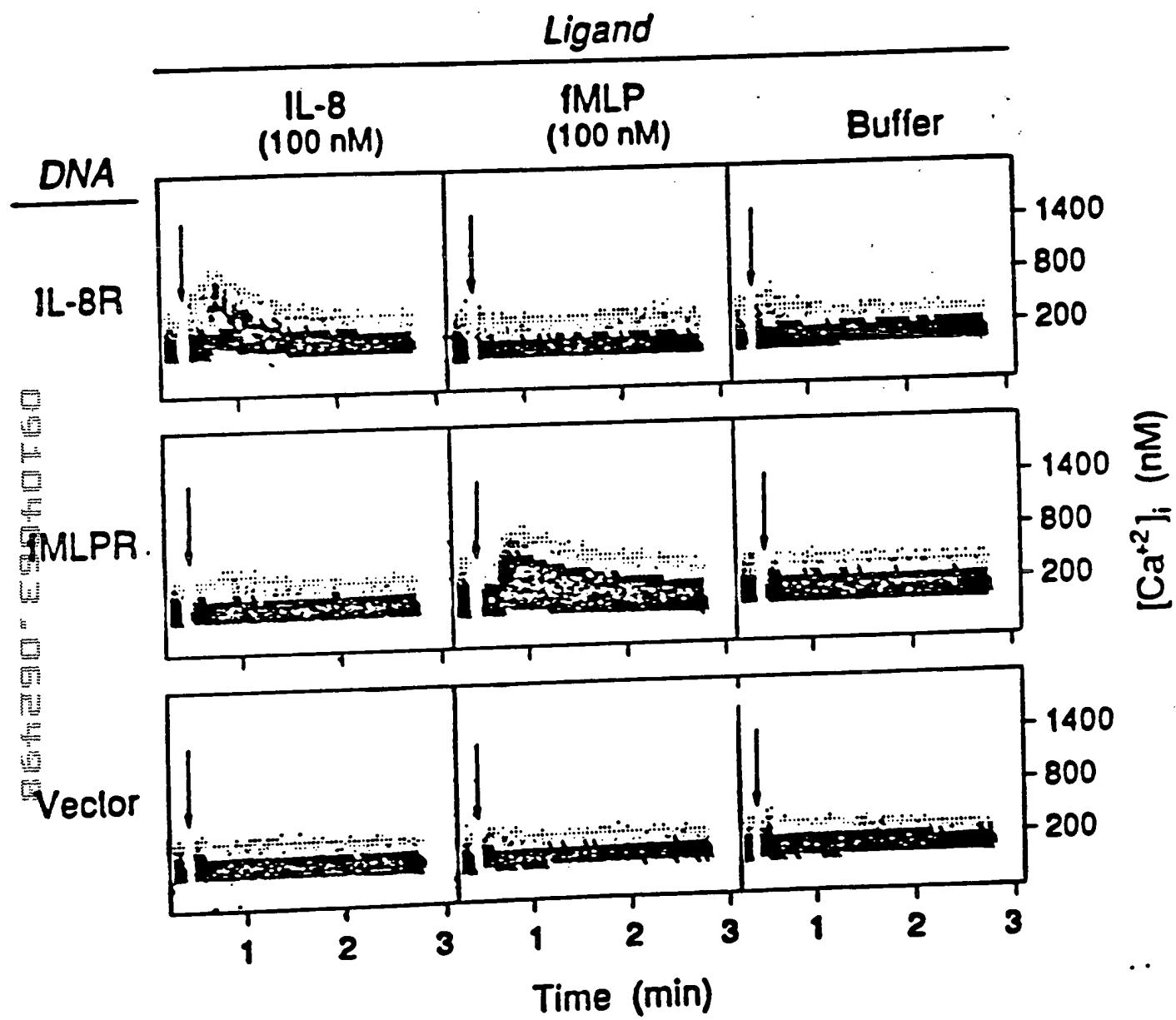


Figure 3a

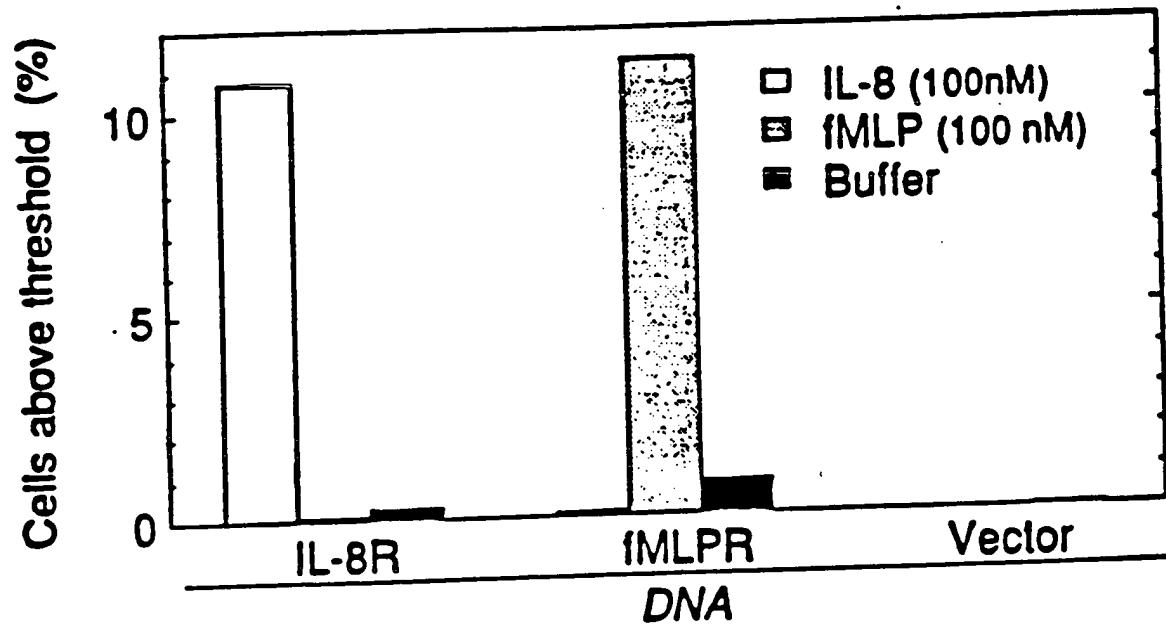


Figure 3b

GAATTCCAGT GTGCTGGCGG CGCGGCGCAA AGTGACGCCG AGGGCCTGAG 50

TGCTCCAGTA GCCACCGCAT CTGGAGAACCC AGCGGTTACC ATG GAG 96
Met Glu
1

GGG ATC AGT ATA TAC ACT TCA GAT AAC TAC ACC GAG GAA 135
Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu
5 10 15

ATG GGC TCA GGG GAC TAT GAC TCC ATG AAG GAA CCC TGT 174
Met Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys
20 25

TTC CGT GAA GAA AAT GCT AAT TTC AAT AAA ATC TTC CTG 213
Phe Arg Glu Glu Asn Ala Asn Phe Asn Lys Ile Phe Leu
30 35 40

CCC ACC ATC TAC TCC ATC ATC TTC TTA ACT GGC ATT GTG 252
Pro Thr Ile Tyr Ser Ile Ile Phe Leu Thr Gly Ile Val
45 50

GGC AAT GGA TTG GTC ATC CTG GTC ATG GGT TAC CAG AAG 291
Gly Asn Gly Leu Val Ile Leu Val Met Gly Tyr Gln Lys
55 60 65

AAA CTG AGA AGC ATG ACG GAC AAG TAC AGG CTG CAC CTG 330
Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
70 75 80

TCA GTG GCC GAC CTC CTC TTT GTC ATC ACG CTT CCC TTC 369
Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe
85 90

TGG GCA GTT GAT GCC GTG GCA AAC TGG TAC TTT GGG AAC 408
Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn
95 100 105

TTC CTA TGC AAG GCA GTC CAT GTC ATC TAC ACA GTC AAC 447
Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn
110 115

CTC TAC AGC AGT GTC CTC ATC CTG GCC TTC ATC AGT CTG 486
Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu
120 125 130

GAC CGC TAC CTG GCC ATC GTC CAC GCC ACC AAC AGT CAG 525
Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln
135 140 145

AGG CCA AGG AAG CTG TTG GCT GAA AAG GTG GTC TAT GTT 564
Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val
150 155

GGC GTC TGG ATC CCT GCC CTC CTG CTG ACT ATT CCC GAC 603
Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp
160 165 170

Figure 4a

D
S
P
D
G
W
-
D
G
E
G
D
G

TTC ATC TTT GCC AAC GTC AGT GAG GCA GAT GAC AGA TAT 642
Phe Ile Phe Ala Asn Val Ser Glu Ala Asp Asp Arg Tyr
175 180

ATC TGT GAC CGC TTC TAC CCC AAT GAC TTG TGG GTG GTT 681
Ile Cys Asp Arg Phe Tyr Pro Asn Asp Leu Trp Val Val
185 190 195

GTG TTC CAG TTT CAG CAC ATC ATG GTT GGC CTT ATC CTG 720
Val Phe Gln Phe Gln His Ile Met Val Gly Leu Ile Leu
200 205 210

CCT GGT ATT GTC ATC CTG TCC TGC TAT TGC ATT ATC ATC 759
Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile
215 220

TCC AAG CTG TCA CAC TCC AAG GGC CAC CAG AAG CGC AAG 798
Ser Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys
225 230 235

GCC CTC AAG ACC ACA GTC ATC CTC ATC CTG GCT TTC TTC 837
Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
240 245

GCC TGT TGG CTG CCT TAC TAC ATT GGG ATC AGC ATC GAC 876
Ala Cys Trp Leu Pro Tyr Tyr Ile Gly Ile Ser Ile Asp
250 255 260

TCC TTC ATC CTC CTG GAA ATC ATC AAG CAA GGG TGT GAG 915
Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln Gly Cys Glu
265 270 275

TTT GAG AAC ACT GTG CAC AAG TGG ATT TCC ATC ACC GAG 954
Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
280 285

GCC CTA GCT TTC TTC CAC TGT TGT CTG AAC CCC ATC CTC 993
Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu
290 295 300

TAT GCT TTC CTT GGA GCC AAA TTT AAA ACC TCT GCC CAG 1032
Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln
305 310

CAC GCA CTC ACC TCT GTG AGC AGA GGG TCC AGC CTC AAG 1071
His Ala Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys
315 320 325

ATC CTC TCC AAA GGA AAG CGA GGT GGA CAT TCA TCT GTT 1110
Ile Leu Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val
330 335 340

TCC ACT GAG TCT GAG TCT TCA AGT TTT CAC TCC AGC TAAC 1150
Ser Thr Glu Ser Ser Ser Phe His Ser Ser
345 350 352

ACAGATGTAA AAGACTTTTT TTTATACGAT AAATAACTTT TTTTTAAGTT 1200

ACACATTTT CAGATATAAA AGACTGACCA ATATTGTACA GTTTTTATTG 1250
CTTGTGGAT TTTGTCTTG TGTTTCTTA GTTTTGTGA AGTTAATTG 1300
ACTTATTTAT ATAAATTTT TTTGTTCAT ATTGATGTGT GTCTAGGCAG 1350
GACCTGTGGC CAAGTTCTTA GTTGCTGTAT GTCTCGTGGT AGGACTGTAG 1400
AAAAGGGAAC TGAACATTCC AGAGCGTGTGTA GTGAATCACG TAAAGCTAGA 1450
AATGATCCCC AGCTGTTAT GCATAGATAA TCTCTCCATT CCCGTGGAAC 1500
GTTTTTCTG TTCTTAAGAC GTGATTTGC TGTAGAAGAT GGCACCTATA 1550
ACCAAAAGCCC AAAGTGGTAT AGAAATGCTG GTTTTCAGT TTTCAGGAGT 1600
GGGTTGATT CAGCACCTAC AGTGTACAGT CTTGTATTAA GTTGTAAATA 1650
AAAGTACATG TTAAACTAA AAAAAAAA AAAAAAAA AAAAAAAA 1700
AAAAAAAAAA AAAGCGGCCG CCAGCACACT GGAATTC 1737

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Figure 4c

GAATTCCAGT GTGCTGGCGG CCGCCCCAGTG TGCTGGCGGC GGCAGTTGAG 50
 GGAAAGGACA GAGGTTATGA GTGCCTGCAA GAGTGGCAGC CTGGAGTAGA 100
 GAAAACACTA AAGGTGGAGT CAAAAGACCT GAGTTCAAGT CCCAGCTCTG 150
 CCACTGGTTA GCTGTGGGAT CTCGGAAAAG ACCCAGTGA AAAAAAAAAA 200
 AAAAGTGAATGA GTTGTGAGGC AGGTGGCGGC CCTACTGCCT CAGGAGACGA 250
 TGCGCAGCTC ATTTGCTTAA ATTTGCAGCT GACGGCTGCC ACCTCTCTAG 300
 AGGCACCTGG CGGGGAGCCT CTCACACATAA GACAGTGACC AGTCTGGTGA 350
 CTCACAGCCG GCACAGCC ATG AAC TAC CCG CTA ACG CTG GAA 392
 Met Asn Tyr Pro Leu Thr Leu Glu
 1 5
 ATG GAC CTC GAG AAC CTG GAG GAC CTG TTC TGG GAA CTG 431
 Met Asp Leu Glu Asn Leu Glu Asp Leu Phe Trp Glu Leu
 10 15 20
 GAC AGA TTG GAC AAC TAT AAC GAC ACC TCC CTG GTG GAA 470
 Asp Arg Leu Asp Asn Tyr Asn Asp Thr Ser Leu Val Glu
 25 30
 AAT CAT CTC TGC CCT GCC ACA GAG GGG CCC CTC ATG GCC 509
 Asn His Leu Cys Pro Ala Thr Glu Gly Pro Leu Met Ala
 35 40 45
 TCC TTC AAG GCC GTG TTC GTG CCC GTG GCC TAC AGC CTC 548
 Ser Phe Lys Ala Val Phe Val Pro Val Ala Tyr Ser Leu
 50 55 60
 ATC TTC CTC CTG GGC GTG ATC GGC AAC GTC CTG GTG CTG 587
 Ile Phe Leu Leu Gly Val Ile Gly Asn Val Leu Val Leu
 65 70
 GTG ATC CTG GAG CGG CAC CGG CAG ACA CGC AGT TCC ACG 626
 Val Ile Leu Glu Arg His Arg Gln Thr Arg Ser Ser Thr
 75 80 85
 GAG ACC TTC CTG TTC CAC CTG GCC GTG GCC GAC CTC CTG 665
 Glu Thr Phe Leu Phe His Leu Ala Val Ala Asp Leu Leu
 90 95
 CTG GTC TTC ATC TTG CCC TTT GCC GTG GCC GAG GGC TCT 704
 Leu Val Phe Ile Leu Pro Phe Ala Val Ala Glu Gly Ser
 100 105 110

Figure 5a

GTG GGC TGG GTC CTG GGG ACC TTC CTC TGC AAA ACT GTG 743
 Val Gly Trp Val Leu Gly Thr Phe Leu Cys Lys Thr Val
 115 120 125

 ATT GCC CTG CAC AAA GTC AAC TTC TAC TGC AGC AGC CTG 782
 Ile Ala Leu His Lys Val Asn Phe Tyr Cys Ser Ser Leu
 130 135

 CTC CTG GCC TGC ATC GCC GTG GAC CGC TAC CTG GCC ATT 821
 Leu Leu Ala Cys Ile Ala Val Asp Arg Tyr Leu Ala Ile
 140 145 150

 GTC CAC GCC GTC CAT GCC TAC CGC CAC CGC CGC CTC CTC 860
 Val His Ala Val His Ala Tyr Arg His Arg Arg Leu Leu
 155 160

 TCC ATC CAC ATC ACC TGT GGG ACC ATC TGG CTG GTG GGC 899
 Ser Ile His Ile Thr Cys Gly Thr Ile Trp Leu Val Gly
 165 170 175

 TTC CTC CTT GCC TTG CCA GAG ATT CTC TTC GCC AAA GTC 938
 Phe Leu Leu Ala Leu Pro Glu Ile Leu Phe Ala Lys Val
 180 185 190

 AGC CAA GGC CAT CAC AAC AAC TCC CTG CCA CGT TGC ACC 977
 Ser Gln Gly His His Asn Asn Ser Leu Pro Arg Cys Thr
 195 200

 TTC TCC CAA GAG AAC CAA GCA GAA ACG CAT GCC TGG TTC 1016
 Phe Ser Gln Glu Asn Gln Ala Glu Thr His Ala Trp Phe
 205 210 215

 ACC TCC CGA TTC CTC TAC CAT GTG GCG GGA TTC CTG CTG 1055
 Thr Ser Arg Phe Leu Tyr His Val Ala Gly Phe Leu Leu
 220 225

 CCC ATG CTG GTG ATG GGC TGG TGC TAC GTG GGG GTA GTG 1094
 Pro Met Leu Val Met Gly Trp Cys Tyr Val Gly Val Val
 230 235 240

 CAC AGG TTG CGC CAG GCC CAG CGG CGC CCT CAG CGG CAG 1133
 His Arg Leu Arg Gln Ala Gln Arg Arg Pro Gln Arg Gln
 245 250 255

 AAG GCA GTC AGG GTG GCC ATC CTG GTG ACA AGC ATC TTC 1172
 Lys Ala Val Arg Val Ala Ile Leu Val Thr Ser Ile Phe
 260 265

 TTC CTC TGC TGG TCA CCC TAC CAC ATC GTC ATC TTC CTG 1211
 Phe Leu Cys Trp Ser Pro Tyr His Ile Val Ile Phe Leu
 270 275 280

 GAC ACC CTG GCG AGG CTG AAG GCC GTG GAC AAT ACC TGC 1250
 Asp Thr Leu Ala Arg Leu Lys Ala Val Asp Asn Thr Cys
 285 290

Figure 5b

GAG TTC CTG GGC CTG GCC CAC TGC TGC CTC AAC CCC ATG 1328
 Glu Phe Leu Gly Leu Ala His Cys Cys Leu Asn Pr Met
 310 315 320

CTC TAC ACT TTC GCC GGC GTG AAG TTC CGC AGT GAC CTG 1367
 Leu Tyr Thr Phe Ala Gly Val Lys Phe Arg Ser Asp Leu
 325 330

TCG CGG CTC CTG ACG AAG CTG GGC TGT ACC GGC CCT GCC 1406
 Ser Arg Leu Leu Thr Lys Leu Gly Cys Thr Gly Pro Ala
 335 340 345

TCC CTG TGC CAG CTC TTC CCT AGC TGG CGC AGG AGC AGT 1445
 Ser Leu Cys Gln Leu Phe Pro Ser Trp Arg Arg Ser Ser
 350 355

CTC TCT GAG TCA GAG AAT GCC ACC TCT CTC ACC ACG TTC TA 1486
 Leu Ser Glu Ser Glu Asn Ala Thr Ser Leu Thr Thr Phe
 360 365 370 372

GGTC CCAGTGTCCC CTTTTATTGC TGCTTTCTT TGGGGCAGGC 1530

AGT GAT GCTG GAT GCT CCTT CCAACAGGGAG CTGGGATCCT AAGGGCTCAC 1580

CGGGCTAAG AGTGTCTAG GAGTATCCTC ATTTGGGGTA GCTAGAGGAA 1630

CCAACCCCCA TTCTAGAAC ATCCCGCGGC CGCCAGCACA CTGGAATTC 1679

09104063 062445

Figure 5c

Receptor Structure of Human IL-8R

$$\text{NH}_2-\text{WESNITDQDQWMDF}$$

DEDAAPPNGTEN 20

CELESTE

2

39

3

1

1

1

11

134

10

३४

A

EIGEN

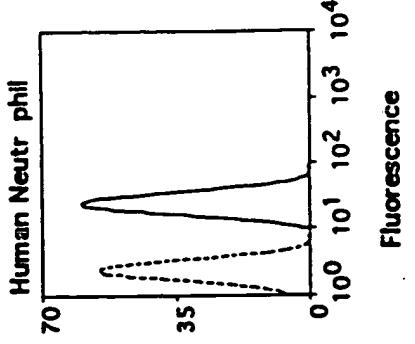
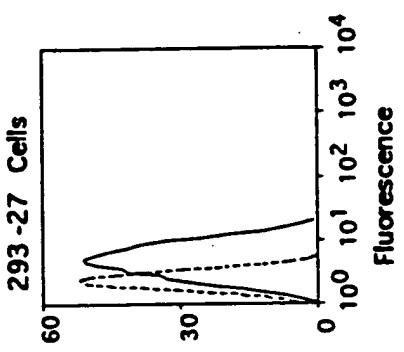
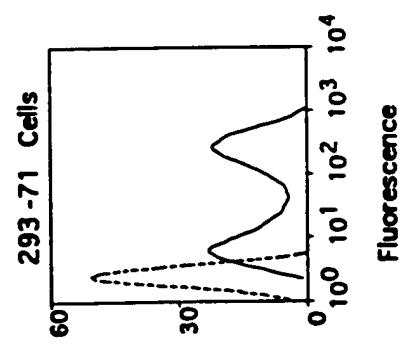
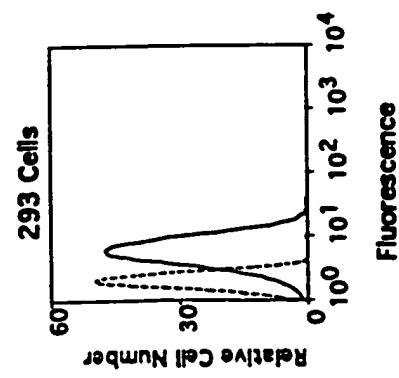


FIG. 8

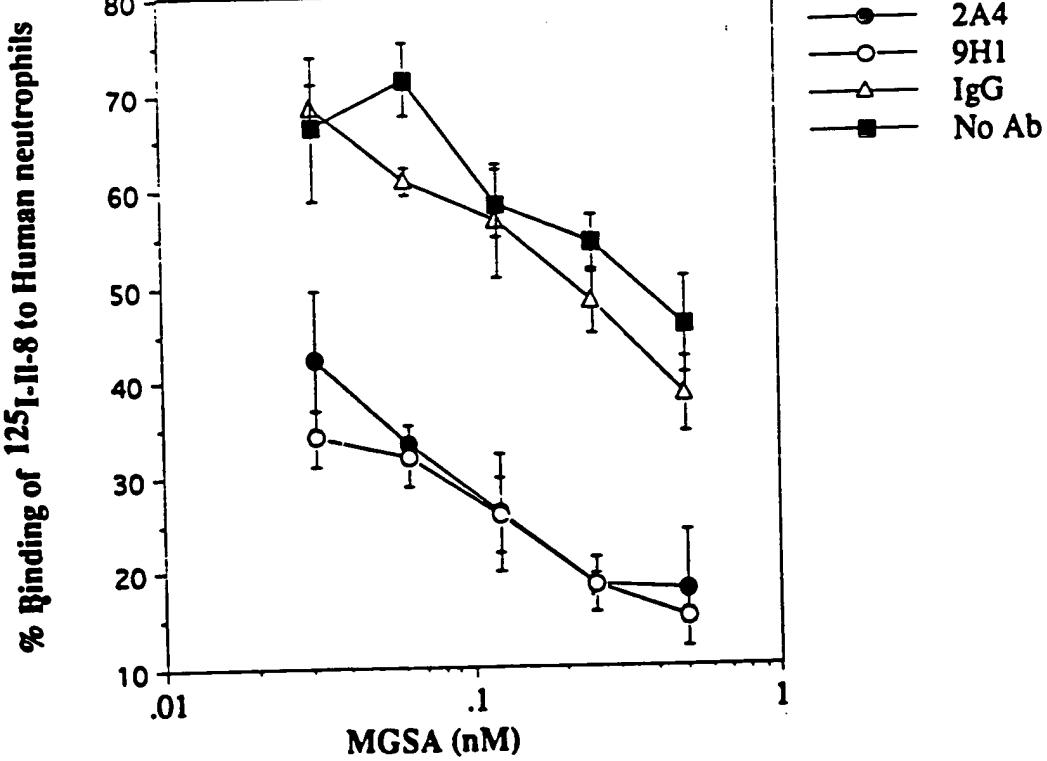
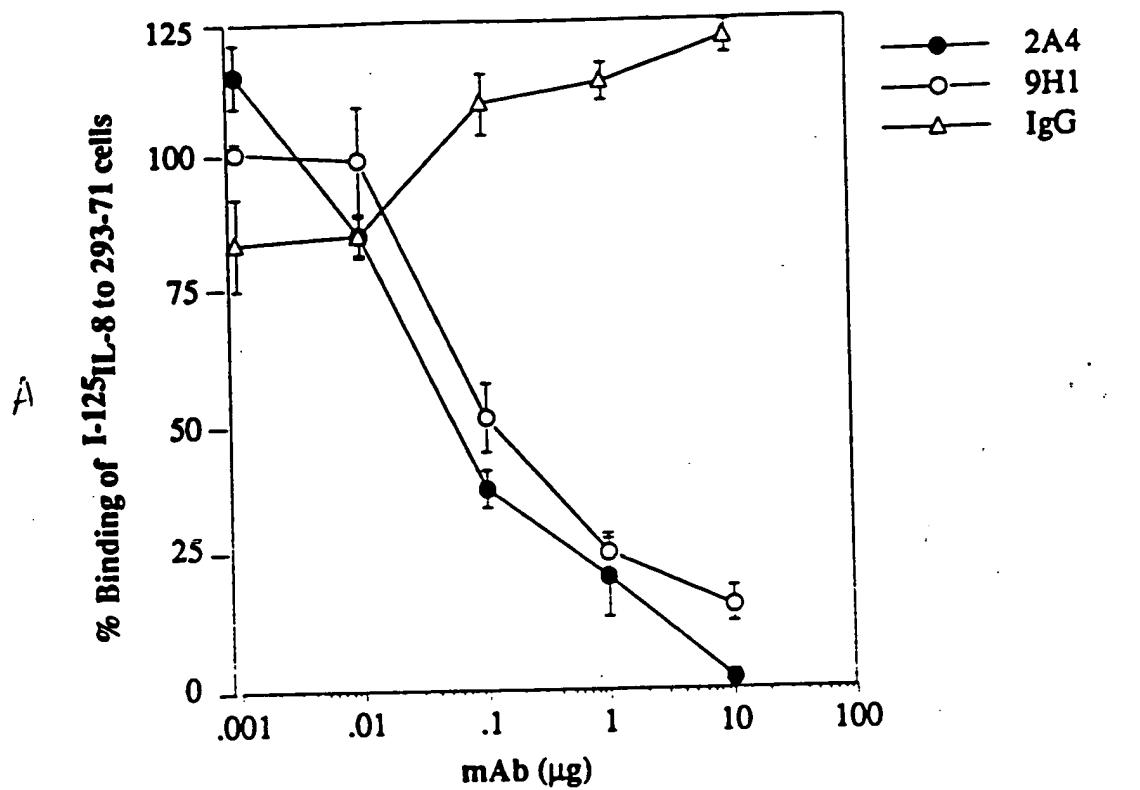
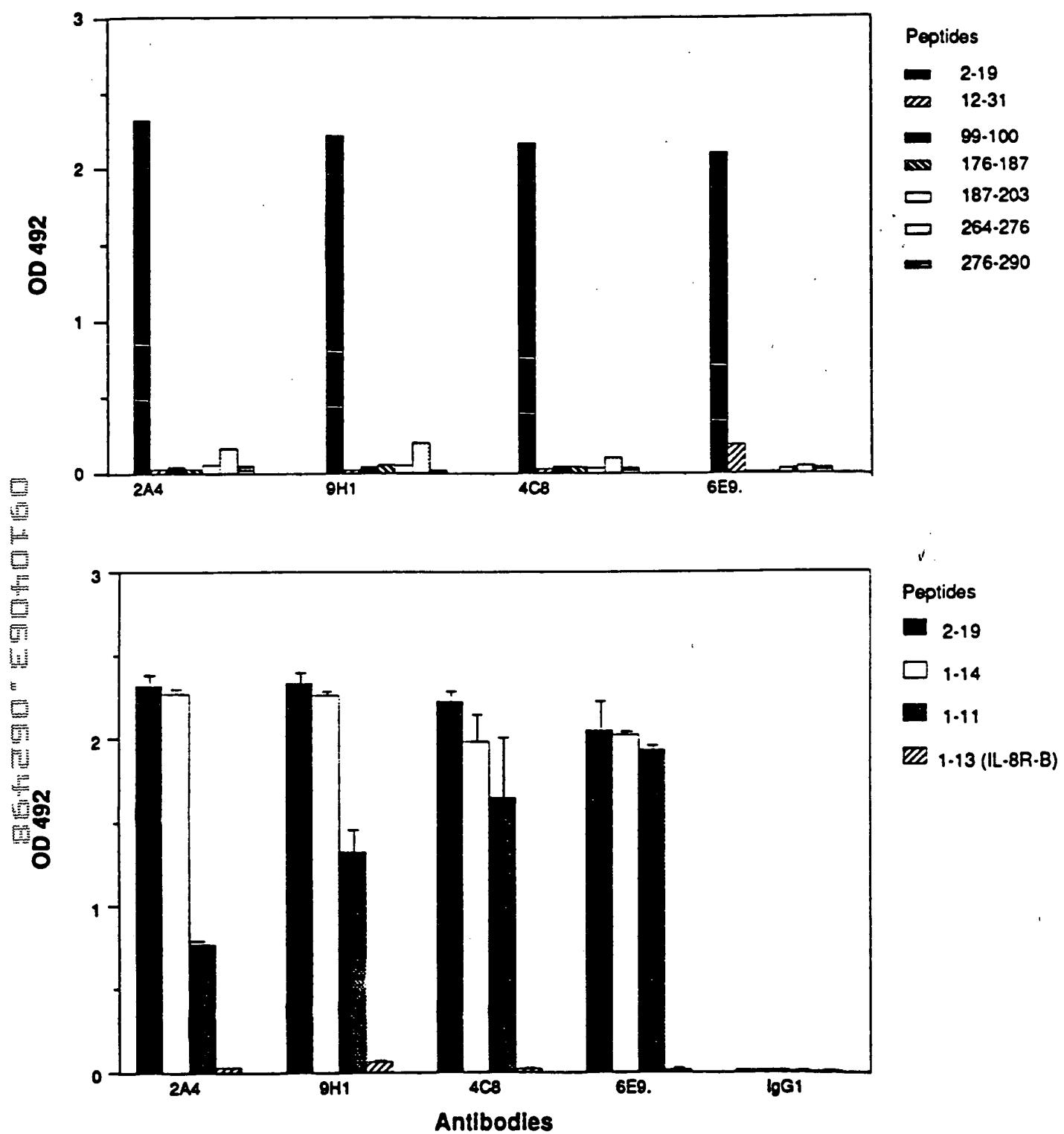


FIG 4



Concentrations of IL-8 in Sputum from Patients with Chronic Airway Inflammation and Induced Sputum from Healthy Subjects

